

SEQUENCE LISTING

6180768

(1) GENERAL INFORMATION:

- (i) APPLICANT: MAERTENS, GEERT
STUYVER, LIEVEN
- (ii) TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
AGENTS
- (iii) NUMBER OF SEQUENCES: 207
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: ARNOLD, WHITE & DURKEE
 - (B) STREET: P.O. BOX 4433
 - (C) CITY: HOUSTON
 - (D) STATE: TEXAS
 - (E) COUNTRY: USA
 - (F) ZIP: 77210-4433
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Microsoft Word 6.0 / ASCII text output
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/836,075
 - (B) FILING DATE: 21 Apr 1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/EP95/04155
 - (B) FILING DATE: 23 Oct 1995
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: EP 94870166.9
 - (B) FILING DATE: 21 Oct 1994
- (ix) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: EP 95870076.7
 - (B) FILING DATE: 28 Jun 1995
- (x) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: KAMMERER, PATRICIA A.
 - (B) REGISTRATION NUMBER: 29,775
 - (C) REFERENCE/DOCKET NUMBER: INNS:004

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCTCAK	60
GGSGTNNNNN NNCCGGGTGG CGGTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCGCAGG	120
GGCCCCAGGN NGGGTGTGCG CGCGACTAGG AAGACTTCCG AGCGGTACAA ACCTCGTGGC	180
AGGCGACAGC CTATCCCCAA GGCTCGYCGG YCCGAGGGCA GGTCCCTGGGC TCAGCCCCGG	240
TATCCTTGGC CCCTCTATGG CAATGAGGGC TGCGGGTGGG CGGGNTGGCT CCTGTCCCCC	300
CGCGGCTCTC GGCCCAATTG GGGCCCC	327

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn			
1	5	10	15

Arg Arg Pro Xaa Xaa Xaa Xaa Pro Gly Gly Gly Gln Ile Val Gly			
20	25	30	

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Xaa Gly Val Arg Ala			
35	40	45	

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	

Ile Pro Lys Ala Xaa Arg Xaa Glu Gly Arg Ser Trp Ala Gln Pro Gly			
65	70	75	80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Xaa Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro
100 105

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GACGGCGTGA ACTATGCAAC AGGGAACCTTG CCCGGTTGCT CTTTCTCTAT CTTCTCTTG	60
GCTTTGCTGT CCTGCTTGAC GGTTCCAACK ACCGCTCACG AGGTGCGCAA CGCATCCGGG	120
GTGTATCATG TCACCAACGA CTGTTCCAAC TCGAGCATCA TCTATGAGAT GGACGGTATG	180
ATCATGCACT ACCCAGGGTG CGTGCCCTGC GTTCGGGAGG ATAACCATCT CCGCTGCTGG	240
ATGGCGCTCA CCCCCACGCT TGCGGTCAAA AAYGCTAGTG TCCCCACTRC GGCAATCCGA	300
CGTCACGTCG ACTTGCTTGT TGGGGNNNCC ACGTTCTGTT CCGCTATGTA CGTGGGRGAC	360
CTTTGCGGGT CTGTCTTCCT CGCTGGCCAG CTATTACCTT TTTCACCCCG CATGCACCAT	420
ACAAACGCAGG AGTGCAACTG CTCAATC	447

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser

1	5	10	15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Xaa Thr Ala			
20	25	30	
His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp Cys			
35	40	45	
Ser Asn Ser Ser Ile Ile Tyr Glu Met Asp Gly Met Ile Met His Tyr			
50	55	60	
Pro Gly Cys Val Pro Cys Val Arg Glu Asp Asn His Leu Arg Cys Trp			
65	70	75	80
Met Ala Leu Thr Pro Thr Leu Ala Val Lys Xaa Ala Ser Val Pro Thr			
85	90	95	
Xaa Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Xaa Xaa Thr Phe			
100	105	110	
Cys Ser Ala Met Tyr Val Xaa Asp Leu Cys Gly Ser Val Phe Leu Ala			
115	120	125	
Gly Gln Leu Phe Thr Phe Ser Pro Arg Met His His Thr Thr Gln Glu			
130	135	140	
Cys Asn Cys Ser Ile			
145			

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAACGTA ACACCAACCG CCGCCCACAG	60
GACGTCAAGN TCCCGGGTGG TGGTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGACCAGG AAGACTTCCG AGCGGTGCGA GCCTCGTGAC	180
AGGCGACAGC CTATTCTAA GGCTCGCCAG TCCGATGGCA GNNCCTGGGC TCAGCCAGGG	240

CATCCCTGGC CCCTCTATGG CAATGAGGGC TCGGGATGGG CGGGATGGCT CCTGTCCCCC 300
CGCGGCTCTC GGCCCAGTTG GGGCCCCC 327

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	
Arg	Arg	Pro	Gln	Asp	Val	Lys	Xaa	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
					20				25					30	
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala
						35			40					45	
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Asp	Arg	Arg	Gln	Pro
						50			55					60	
Ile	Pro	Lys	Ala	Arg	Gln	Ser	Asp	Gly	Xaa	Xaa	Trp	Ala	Gln	Pro	Gly
						65			70			75			80
His	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp
						85			90					95	
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro			
						100			105						

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - iii) HYPOTHETICAL: NO
 - iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GACGGCGTGA ACTATGCAAC AGGGAATTG CCTGGTTGCT CTTTCTCTAT CTTCCCTTTA	60
GCTTTCTGT CCTGCTTGAC GGTTCCAATC ACCGCTCATG AGGTGCGCAA CGCATCCGGG	120
GTATATCATC TCACCAATGA CTGTTCCAAC TCGAGCATCA TCTATGAGAT GAGTGGTATG	180
ATCTTGCACG CCCCAGGGTG TGTGCCCTGC GTTCGGGAGA ACAACTCTTC TCGTTGCTGG	240
ATGCCRCTCA CCCCCACGCT TGCGGTCAAA GACGCTAATG TCCCTACTGC GGCAATCCGA	300
CGCCATGTCTG ACTTGCTGGT TGGGACAGCC GCGTTTCGTT CCGCTATGTA CGTGGGGGAC	360
CTCTGCGGAT CCGTCTTCCT TGTCGGCCAG CTATTCACCT TTTCACCCCG CTTGTACCAT	420
ACAAACACAGG AGTGCAACTG CTCAATC	447

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser			
1	5	10	15
Ile Phe Leu Leu Ala Phe Leu Ser Cys Leu Thr Val Pro Thr Thr Ala			
20	25	30	
His Glu Val Arg Asn Ala Ser Gly Val Tyr His Leu Thr Asn Asp Cys			
35	40	45	
Ser Asn Ser Ser Ile Ile Tyr Glu Met Ser Gly Met Ile Leu His Ala			
50	55	60	
Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp			
65	70	75	80
Met Xaa Leu Thr Pro Thr Leu Ala Val Lys Asp Ala Asn Val Pro Thr			
85	90	95	
Ala Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Thr Ala Ala Phe			
100	105	110	
Arg Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val			

115	120	125
Gly Gln Leu Phe Thr Phe Ser Pro Arg Leu Tyr His Thr Thr Gln Glu		
130	135	140
Cys Asn Cys Ser Ile		
145		

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA ACACCAACCG CCGCCCACAG	60
GACGTCAAGT TCCCGGGCGG TGGCCAGATC GTTGGTGGAG TCTACGTGCT ACCGCGCAGG	120
GGCCCTAGAT TGGGTGTGCG CGCAGCGCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG	180
AGGCGCCAAC CTATTCCCAA GGAGCGCCGA CCCGAGGGCA GGT	223

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn		
1	5	10
		15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly		
20	25	30

Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala

35

40

45

Ala Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

Ile Pro Lys Glu Arg Arg Pro Glu Gly Arg
 65 70

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAACGCA ACACCAACCG CCGCCCACAG	60
GACGTTAAAT TCCCAGGTGG GGGCAGATC GTGGGTGGAG TTTACTTGTGTT GCCGCGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGACGAGG AAGACTTCCG AGCGGTGCGA ACCTCGCGGA	180
AGGCGACAGC CTATCCCCAA GGCTCGCCGA CCCGAGGGCA GGTCTGGGC TCAGCCTGGG	240
TACCCATGGC CCCTCTATGC TAACGAGGGC TGCGGATGGG CGGGATGGCT CCTGTCCCCT	300
CGCGGCTCCC GTCCTAGCTG GGGCCCCAAT GACCCCCGAC GTAGATCACG CAATTGGGT	360
AAGGTCATCG ATACCCTAAC GTGTGGCTTC GCCGATCTCA TGGGGTACAT TCCGCTCGTC	420
GGCGCCCCCCC TAGGGGGCGC TTCCAGAACCT CTGNCACATG GTGTCCGGGT CCTGGNAGGC	480
GGCGTGATNN NNNNNNNNNN NAACCTTCNN GGTTGCTCTT TNNCTATCTT CCTCTTGGCN	540
TTACTCTCTT GCCTCACAGT CCCCCACCTCT GCCTATGAGG TGCACAGCAC AACCGATGGC	600
TACCATGTCA CTAATGACTG TTCCAACGGC AGCATCGTAT ATGAGGCAAA GGACATCATC	660
CTTCACACGC CTGGGTGNGT GCCCTGCATA CGGGAAGGCA ATATCTCCG TTGCTGGTA	720
CCGCTCACCC CCACGCTCGC AGCGCGGATC GCGAACGCTC CCATCGATGA GGTGCGGGGT	780
CACGTCGACC TCCTCGTGGG GGCAGCCGTG TTCTGCTCAG CCATGTACAT TGGGGACCTT	840

TGTGGGGCG TCTTCCTCGT TGGGCAATTG TTCACCTTCA CGTCCCGGCG GCATTGGACG 900

GTGCAGGACT GTAATTGTTCA CATTACTCT GGCCACATAA CGGGCCACCG NNNNNNN 957

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
130 135 140

Gly Gly Ala Ser Arg Thr Leu Xaa His Gly Val Arg Val Leu Xaa Gly
145 150 155 160

Gly Val Xaa Xaa Xaa Xaa Asn Leu Xaa Gly Cys Ser Xaa Xaa Ile
165 170 175

Phe Leu Leu Xaa Leu Leu Ser Cys Leu Thr Val Pro Thr Ser Ala Tyr
180 185 190

Glu Val His Ser Thr Thr Asp Gly Tyr His Val Thr Asn Asp Cys Ser

195	200	205
Asn Gly Ser Ile Val Tyr Glu Ala Lys Asp Ile Ile Leu His Thr Pro		
210	215	220
Gly Xaa Val Pro Cys Ile Arg Glu Gly Asn Ile Ser Arg Cys Trp Val		
225	230	235
Pro Leu Thr Pro Thr Leu Ala Ala Arg Ile Ala Asn Ala Pro Ile Asp		
245	250	255
Glu Val Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Val Phe Cys		
260	265	270
Ser Ala Met Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu Val Gly		
275	280	285
Gln Leu Phe Thr Phe Thr Ser Arg Arg His Trp Thr Val Gln Asp Cys		
290	295	300
Asn Cys Ser Ile Tyr Ser Gly His Ile Thr Gly His Xaa Xaa Xaa		
305	310	315

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATGAGCACAA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA ATACCAACCG CCGCCCACAG	60
GACGTCAAGT TCCCAGGGCGG CGGCCAGATC GTTGGCGGAG TTTACTTGTGTT GCCGCGCAGG	120
GGCCCCAGAT TGGGTGTGCG CGCGACGAGA AAGACTTCTG AACGGTCCCA GCCACGTGGA	180
AGGCGCCAGC CCATCCCTAA AGATCGGNGN GCCACTGGCA GGTCTGGGG ACGTCCAGGA	240
TATCCCTGGC CCCTGTATGG GAACGAGGGG CTCGGCTGGG CAGGATGGCT CCTGTCCCCC	300
CGAGGCTCTC	310

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Asp Arg Xaa Ala Thr Gly Arg Ser Trp Gly Arg Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly
100 105

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACGTGCGGNT NTGCCGACCT CATGGGGTAC ATNCCCGTTG TCGGCGCCCC GGTGGGCGGG	60
GTNGCCAGGG CCCTCGCGNA TGGCGTGCAGG GTCCTGGAGG ACGGGATAAA TTATGNAACA	120

GGGAACCTCC	CTGGTTGCTC	CTTTCTATC	TTCTNGTTGG	CTCTTCTGTC	TTGTGTCACC	180
GTGCCTGTCT	CTGNCGTTGA	GGTCAAAAAT	ACCAGTCAGG	CCTATATGGC	AACCAACGAC	240
TGCTCCAACA	ACAGCATCGT	ATGGCAATTG	GNGGACGCGG	TGCTTCATGT	TCCTGGATGT	300
GTCCCCTGCG	AGAATAGCTC	CGGTCGGTTC	CACTGTTGGA	TCCCGATCTC	GCCCAACATA	360
GCCGTGAGCA	AACCTGGTGC	TCTCACCAAG	GGACTGCGGG	CACGCATTGA	TGCCGTCGTG	420
ATGTCCGCCA	CCCTCTGCTC	TGCCCTGTAC	GTGGGAGATG	TGTGCGGCGC	AGTGATGATA	480
GCTGCACAGG	CTTTCATCGT	GGCACCGAAG	CGCCATTACT	TCGTCCAGGA	ATGCAATTGC	540
TCCATATACC	CAGGCCACAT	TACAGGTCAT	CGCATGGCG			579

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Thr	Cys	Xaa	Xaa	Ala	Asp	Leu	Met	Gly	Tyr	Xaa	Pro	Val	Val	Gly	Ala
1															15
Pro	Val	Gly	Gly	Xaa	Ala	Arg	Ala	Leu	Ala	Xaa	Gly	Val	Arg	Val	Leu
				20				25						30	
Glu	Asp	Gly	Ile	Asn	Tyr	Xaa	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe
				35				40						45	
Ser	Ile	Phe	Xaa	Leu	Ala	Leu	Leu	Ser	Cys	Val	Thr	Val	Pro	Val	Ser
				50				55						60	
Xaa	Val	Glu	Val	Lys	Asn	Thr	Ser	Gln	Ala	Tyr	Met	Ala	Thr	Asn	Asp
				65				70						80	
Cys	Ser	Asn	Asn	Ser	Ile	Val	Trp	Gln	Leu	Xaa	Asp	Ala	Val	Leu	His
					85				90					95	
Val	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Ser	Ser	Gly	Arg	Phe	His	Cys
				100				105						110	
Trp	Ile	Pro	Ile	Ser	Pro	Asn	Ile	Ala	Val	Ser	Lys	Pro	Gly	Ala	Leu
					115				120					125	

Thr Lys Gly Leu Arg Ala Arg Ile Asp Ala Val Val Met Ser Ala Thr
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Val Cys Gly Ala Val Met Ile
145 150 155 160

Ala Ala Gln Ala Phe Ile Val Ala Pro Lys Arg His Tyr Phe Val Gln
165 170 175

Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGAGCACAA ATCCTAAACC TCAAAGAAAA ACTAAAAGAA ACACATAACCG TCGCCCACAG	60
GACGTTAAGT TCCCGGGCGG CGGCCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGCCAAGG AAGACTTCTG AACGGTCCCA GCCACGTGGA	180
AGGCGCCAGC CCATCCAAA AGATCGGCGC GCCACTGGCA AGTCCTGGGG ACGTCCAGGA	240
TACCCCTTGGC CCCTGTACGG GAACGAGGGC CTCGGCTGGG CAGGGTGGCT CCTGTCCCCC	300
CGGGGCTCTC GCCCCCTCGTG GGGCCAAAC GACCCCCGGC ACAGGTACG CAACTTGGGT	360
AAGGTCATCG ATACCCTCAC GTGTGGCTTT GSCGACCTCA TGGGGTACAT ACCTGTCGTC	420
GGCGCCCCCTG TGGGCGGCGT TGCCAGAGCC CTCGCGCATG GCGTGCAGGCT CCTGGAGGAC	480
GGGATAAATT ATGCAACAGG GAACTTGCCC GGTTGCTCCT TTTCTATCTT CTTGCTGGCT	540
CTCTTGTCTT GTATCACCGT GCCCGTGTCT GCCATACAGG TTAAGAACAA CAGCCACTTC	600
TACATGGCGA CTAATGACTG TGCCAATGAC AGCATCGTCT GGCAGCTCAG GGACGCGGTG	660

CTCCATGTC	CTGGATGTGT	CCCCTGTGAG	AGGTCAAGGTA	ATAGGACCTT	CTGTTGGACA	720
GCGGTCTCGC	CCAACGTGGC	TGTGAGCCGA	CCTGGTGCTC	TCACTAGAGG	TCTGCGGGCT	780
CACATTGATA	CCATCGTGAT	GTCCGCCACC	CTCTGCTCTG	CCCTATACAT	AGGGGACCTA	840
TGCGGCGCTG	TGATGATAGC	AGCGCAAGTT	GCCGTCGTCT	CACCGCAATA	CCATACTTTT	900
GTCCAGGAAT	GCAACTGCTC	CATATACCCA	GGCCATATCA	CAGGACATCG	AATGGNN	957

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10				15		

Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
				20				25					30		

Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala
					35			40					45		

Pro	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
					50			55					60		

Ile	Pro	Lys	Asp	Arg	Arg	Ala	Thr	Gly	Lys	Ser	Trp	Gly	Arg	Pro	Gly
					65			70			75		80		

Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp
					85				90			95			

Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
					100				105			110			

Arg	His	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys
					115				120			125			

Gly	Phe	Xaa	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Val	Val	Gly	Ala	Pro	Val
					130			135			140				

Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp
					145			150			155		160		

Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175
 Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Ala Ile
 180 185 190
 Gln Val Lys Asn Asn Ser His Phe Tyr Met Ala Thr Asn Asp Cys Ala
 195 200 205
 Asn Asp Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro
 210 215 220
 Gly Cys Val Pro Cys Glu Arg Ser Gly Asn Arg Thr Phe Cys Trp Thr
 225 230 235 240
 Ala Val Ser Pro Asn Val Ala Val Ser Arg Pro Gly Ala Leu Thr Arg
 245 250 255
 Gly Leu Arg Ala His Ile Asp Thr Ile Val Met Ser Ala Thr Leu Cys
 260 265 270
 Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Ile Ala Ala
 275 280 285
 Gln Val Ala Val Val Ser Pro Gln Tyr His Thr Phe Val Gln Glu Cys
 290 295 300
 Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Xaa
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GACGGGGTAA ATTATGCAAC AGGGAATCTG CCTGGTTGCT CTTTCTCTAT CTTCTTGTG	60
GCTCTTCTGT CTTGTGTCAC CGTGCCTGTC TCTGCCGTGC AGGTTAAGAA CACCAGTACC	120
ATGTACATGG CAACCAATGA CTGTTCCAAC AACAGCATCA TCTGGCAAAT GCAGGGCGCG	180

GTGCTTCATG TTCCTGGATG TGTCCCGTGT GAGTTGCAGG GCAATAAGTC CCGGTGCTGG	240
ATACCGGTCA CTCCCAACGT GGCTGTGAAC CAGCCCGGCG CCCTCACTAG GGGCTTGCAG	300
ACGCACATTG ACACCATCGT GATGGTCGCT ACGCTCTGTT CTGCACTCTA CATCGGGGAC	360
GTGTGTGGCG CGGTGATGAT AGCTGCTCAG GTTGTCAATTG TCTCGCCGCA ACATCACAAAC	420
TTTTCCCAGG ATTGCAATTG TTCCATC	447

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser
1															15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Val Thr Val Pro Val Ser Ala															
															30
Val Gln Val Lys Asn Thr Ser Thr Met Tyr Met Ala Thr Asn Asp Cys															
															45
Ser Asn Asn Ser Ile Ile Trp Gln Met Gln Gly Ala Val Leu His Val															
															60
Pro Gly Cys Val Pro Cys Glu Leu Gln Gly Asn Lys Ser Arg Cys Trp															
															80
Ile Pro Val Thr Pro Asn Val Ala Val Asn Gln Pro Gly Ala Leu Thr															
															95
Arg Gly Leu Arg Thr His Ile Asp Thr Ile Val Met Val Ala Thr Leu															
															110
Cys Ser Ala Leu Tyr Ile Gly Asp Val Cys Gly Ala Val Met Ile Ala															
															125
Ala Gln Val Val Ile Val Ser Pro Gln His His Asn Phe Ser Gln Asp															
															140
Cys Asn Cys Ser Ile															
															145

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATGAGCACAA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA ACACTAACCG CCGCCCACAG	60
GACGTTAAGT TCCCGGGCGG TGGCCAGATC GTTGGCGGAG TATACTTGTGTT GCCGCGCAGG	120
GGCCCCCGGT TGGGTGTGCG CGCGACGAGG AAAACTTCCG AACGGTCCCA GCCACGTGGG	180
AGGCGCCAGC CCATCCCTAA AGATCGGCAGC TCCACTGGCA AATCCTGGGG ACGTCCAGGA	240
TACCCCTTGGC CCCTGTATGG GAACGAGGGC CTTGGTTGGG CAGGATGGCT CTTGTCCCCT	300
CGAGGCTCTC	310

(2) INFORMATION FOR SEQ ID NO: 22:

1 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn			
1	5	10	15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Arg Ser Leu Ala			
20	25	30	
Glu Tyr Thr Cys Ala Arg Arg Gly Lys Leu Arg Arg Ser Ser Met Gly			
35	40	45	

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GACGGGATAA ACTACGCAAC AGGGAATCTG CCCGGTTGCT CCTTTCTAT CTTCTTGCTG	60
GCCTTGCTAT CCTGTCTCAC TGTGCCGGCG TCCGCTGTGC AGGTCAAGAA CACCAGCCAC	120
TCTTATATGG TGACCAATGA TTGCTAAAC AGCAGCATTG TCTGGCAGCT TAAGGATGCT	180
GTGCTTCACG TCCCTGGATG TGTTCCATGT GAGAGGCACC AAAATCAGTC TCGCTGCTGG	240
ATACCTGTGA CACCCAATGT GGCCGTGAGC CAACCTGGCG CGCTCACCAAG GGGTTTGCAG	300
ACGCACATTG ACACCATCGT TGCCTCTGCT ACCGTCTGCT CAGCTTTGTA TGTGGGCGAC	360
TTCTGCGGCG CAGTGATGTT GGTCTCTCAA TTTTCATGA TCTCCCCTCA GCACCACATC	420
TTCGTCCAGG ATTGCAACTG CTCGATA	447

(2) INFORMATION FOR SEO ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser
1				5					10					15	
Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala
							20		25				30		
Val	Gln	Val	Lys	Asn	Thr	Ser	His	Ser	Tyr	Met	Val	Thr	Asn	Asp	Cys
							35		40				45		

Ser Asn Ser Ser Ile Val Trp Gln Leu Lys Asp Ala Val Leu His Val
 50 55 60
 Pro Gly Cys Val Pro Cys Glu Arg His Gln Asn Gln Ser Arg Cys Trp
 65 70 75 80
 Ile Pro Val Thr Pro Asn Val Ala Val Ser Gln Pro Gly Ala Leu Thr
 85 90 95
 Arg Gly Leu Arg Thr His Ile Asp Thr Ile Val Ala Ser Ala Thr Val 1
 100 105 110
 Cys Ser Ala Leu Tyr Val Gly Asp Phe Cys Gly Ala Val Met Leu Val
 115 120 125
 Ser Gln Phe Phe Met Ile Ser Pro Gln His His Ile Phe Val Gln Asp
 130 135 140
 Cys Asn Cys Ser Ile
 145

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GACGGGATAA ACTATGCAAC AGGGAACCTG CCTGGTTGCT CCTTTTCTAT CTTCTTACTG 60
 GCCCTGCTTT CTTGCATCAC CGTGCCGGTC TCTGCCGTGC AAGTTGCGAA CCGCAGTGTT 120
 TCTTACATGG TGACCAATGA TTGCTCGAAC AGCAGCATCG TTTGGCAGCT CGAGGAGGCC 180
 GTCCTTCACG TCCCTGGATG TGTTCCCTGT GAGTGGAAAGG ACAACACCTC CCGCTGCTGG 240
 ATACCGGTCA CCCCTAACAT CGCTGTGAGC CAACCTGGCG CGCTTACCAA GGGCCTGCGG 300
 ACACATATTG ACATCATTGT CGCGTCCGCC ACGTTCTGCT CTGCCTTGTG TGTGGG 356

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser
1															15
Ile Phe Leu Leu Ala Leu Ser Cys Ile Thr Val Pro Val Ser Ala															
															30
Val	Gln	Val	Ala	Asn	Arg	Ser	Gly	Ser	Tyr	Met	Val	Thr	Asn	Asp	Cys
															45
Ser	Asn	Ser	Ser	Ile	Val	Trp	Gln	Leu	Glu	Glu	Ala	Val	Leu	His	Val
															50
Pro	Gly	Cys	Val	Pro	Cys	Glu	Trp	Lys	Asp	Asn	Thr	Ser	Arg	Cys	Trp
															60
Ile	Pro	Val	Thr	Pro	Asn	Ile	Ala	Val	Ser	Gln	Pro	Gly	Ala	Xaa	Thr
															85
Lys	Gly	Leu	Arg	Thr	His	Ile	Asp	Ile	Ile	Val	Ala	Ser	Ala	Thr	Phe
															100
Cys	Ser	Ala	Leu	Tyr	Val										
															115

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAACGTA ACACCAACCG CCGCCCCATG

60

GACGTTAAGT TCCCGGGTGG TGGCCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGACTCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG	180
AGACGCCAAC CTATCCCCAA GGCGCGTCGA TCCGAGGGAA GGTCCTGGGC ACAGGCCAGGA	240
TATCCATGGC CTCTTTACGG TAATGAGGGT TGCGGGTGGG CANNATGGCT CTTGTCCCCC	300
CGCGGTTCTC	310

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	

Arg	Arg	Pro	Met	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
			20				25						30		

Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala
			35			40						45			

Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
	50				55				60						

Ile	Pro	Lys	Ala	Arg	Arg	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly
65				70					75				80		

Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Xaa	Trp
				85				90				95			

Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
			100				105					110			

Arg Arg Arg Ser Arg
115

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GACGGGATCA ATTTTGCAAC AGGGAACCTC CCCGGTTGCT CCTTTCTAT CTTCTCTTG	60
GCACTCCTCT CGTGCCTGAC TGTCCCCGCT TCGGCCATCA ACTATCGCAA TGTCTCGGGC	120
ATTTACTATG TCACCAATGA TTGCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC	180
ATCTTGACCC TCCCAGGTTG CGTGCCTGC GTGAGAGAGG GGAATCAGTC ACGTTGCTGG	240
GTAGCCCTTA CCCCTACCGT CGCAGCGCCA TACATCGGCG CGCCACTTGA GTCTCTACGG	300
AGTCATGTGG ACTTGATGGT GGGGGCCGCC ACTGTTTGTT CAGCCCTTTA CATGGGGAT	360
TTRTGTGGY GCTTGTTCCT AGTCGGTCAG ATGTTCTCTT TCCGACCAAG GCGCCACTGG	420
ACTACTCAAG ATTGCAATTG TTCCATC	447

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30

Ile Asn Tyr Arg Asn Val Ser Gly Ile Tyr Tyr Val Thr Asn Asp Cys
35 40 45

Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
 50 55 60

Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Gln Ser Arg Cys Trp
65 70 75 80

Val	Ala	Leu	Thr	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Ile	Gly	Ala	Pro	Leu	
														85	90	95
Glu	Ser	Leu	Arg	Ser	His	Val	Asp	Leu	Met	Val	Gly	Ala	Ala	Thr	Val	
														100	105	110
Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Xaa	Cys	Xa	Gly	Leu	Phe	Leu	Val	
														115	120	125
Gly	Gln	Met	Phe	Ser	Phe	Arg	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Asp	
														130	135	140
Cys	Asn	Cys	Ser	Ile												
															145	

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GACGGGATCA	ATTATGCAAC	AGGAAACCTT	CCCGGTTGCT	CTTTTTCTAT	CTTCCTCTTG	60
GCACTCCTCT	CGTGCCTGAC	TGTTCCCGCT	TCGGCCATTA	ACTACCGCAA	CACCTCGGGC	120
ATCTACCACG	TCACCAATGA	CTGCCCGAAC	TCGAGCATAG	TTTATGAGGC	CGACCACCAC	180
ATCTTGCACC	TTCCAGGTTG	CGTGCCTGTC	GTGAGAACTG	GGAATCAGTC	ACGTTGCTGG	240
GTGGCCCTTA	CTCCTACCGT	CGCAGCGCCA	TACATCGGCG	CACCGCTTGA	GTCTCTGCGG	300
AGTCATGTGG	ATCTGATGGT	GGGGGCTGCC	ACTGTTGCT	CAGCCCTTA	CATCGGGGAT	360
TTGTGTGGCG	GCTTGTCTT	GGTTGGTCAG	ATGTTTCTT	TCCGACCACCG	ACGCCACTGG	420
ACTGCCCAGG	ATTGCAATTG	TTCTATC				447

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30

Ile Asn Tyr Arg Asn Thr Ser Gly Ile Tyr His Val Thr Asn Asp Cys
35 40 45

Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
50 55 60

Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys Trp
65 70 75 80

Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu
85 90 95

Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
100 105 110

Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu Val
115 120 125

Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Ala Gln Asp
130 135 140

Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GACGGGATTA ATTATGCAAC AGGGAATCTT CCCGGTTGCT CCTTTCTAT CTTCTCTTG 60
GCACTTCTCT CGTGCCTGAC TGTCCCCGCT TCGGCCATTA ACTACCACAA CACCTCGGGC 120
ATCTATCATA TCACCAACGA CTGCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC 180
ATCTTGCATC TCCCAGGTTG CGTGCCTGC GTGAGAGTGG GGAATCAGTC GAGTTGCTGG 240
GTGGCCCTTA CCCCTACCAT CGCAGCGCCA TACATCGGCG CACCGCTTGA GTCCTTGC GG 300
AGTCATGTGG ATCTGATGGT GGGGGCGGCC ACTGTCTGTT CAGCCCTTTA CATCGGGGAT 360
TTGTGTGGCG GTGCGTTCTT GGTTGGTCAG ATGTTCTCTT TCCGACCACG GCGCCACTGG 420
ACCACCCAAG ATTGCAACTG CTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30
Ile Asn Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp Cys
35 40 45
Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
50 55 60
Pro Gly Cys Val Pro Cys Val Arg Val Gly Asn Gln Ser Ser Cys Trp
65 70 75 80
Val Ala Leu Thr Pro Thr Ile Ala Ala Pro Tyr Ile Gly Ala Pro Leu
85 90 95
Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
100 105 110
Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ala Phe Leu Val

115

120

125

Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Asp
130 135 140

Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GACGGGATCA ATTATGCAAC AGGGAATATT CCCGGTTGCT CYTTTTCTAT CTTCCCTTYTG	60
GCACTTCTCT CGTGCTTGAC TGTCCCCGCT TCGGCCACTA ACTATCGCAA CGTCTCGGGC	120
ATCTACCATG TCACCAATGA CTGCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC	180
ATCTTAGCAC TTCCAGGTTG CGTGCCCTGC GTGAGAGTGG GGAACCAGTC ACGCTGCTGG	240
GTGGCCCTTA CCCCTACCGT CGCAGCGCCA TACACCGCGG CGCCGCTTGA GTCCCTGCGG	300
AGTCATGTGG ATCTGATGGT GGGAGCTGCC ACTGTTGTT CAGCCCTTA CATGGGGAY	360
TTGTGTGGCG GCTTGTCTT GGTTGGTCAG ATGTTCTCTT TYCAGCCTCG GCGCCACTGG	420
ACTACCCAGG ATTGCAATTG TTCCATC	447

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Ile Pro Gly Cys Xaa Phe Ser
 1 5 10 15
 Ile Phe Leu Xaa Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
 20 25 30
 Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
 35 40 45
 Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu Ala Leu
 50 55 60
 Pro Gly Cys Val Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys Trp
 65 70 75 80
 Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Thr Ala Ala Pro Leu
 85 90 95
 Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
 100 105 110
 Cys Ser Ala Leu Tyr Ile Gly Xaa Leu Cys Gly Gly Leu Phe Leu Val
 115 120 125
 Gly Gln Met Phe Ser Xaa Gln Pro Arg Arg His Trp Thr Thr Gln Asp
 130 135 140
 Cys Asn Cys Ser Ile
 145

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GACGGGATTA ATTATGCAAC AGGAAAYCTC CCCGGTTGCT CTTTTTCTAT CTTCCTCTTG	60
GCACTTCTCT CGTGCCTGAC TGTCCCCGCT TCGGCCACCA ACTACCGCAA TGTCTCGGGC	120
ATTTACCATG TCACCAATGA CTGCCCGAAT TCAAGCATAG TGTTTGAGGC CGACCATCAC	180

ATCTTGCACC TTCCAGGATG CGTGCCTGC GTGAAAGAGG GAAATCATTC ACGCTGCTGG	240
GTGGCCCTTA CCCCTACCGT CGCAGCGCCA TACATCGGCG CGCCACTTGA GTCTCTACGG	300
AGTCATGTGG ATGTGATGGT GGGGGCTGCC ACTGTTGTT CAGCCCTTA CATCGGGAT	360
CTGTGCGGTG GCTTGGTCCT GGTTGGTCAG ATGTTCTCTT TCCGACCACG GCGCCACTGG	420
ACTACCCAGG AATGCAATTG TTCCATC	447

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Asp Gly Ile Asn Tyr Ala Thr Gly Xaa Leu Pro Gly Cys Ser Phe Ser
1 5 10 15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30

Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
35 40 45

Pro Asn Ser Ser Ile Val Phe Glu Ala Asp His His Ile Leu His Leu
50 55 60

Pro Gly Cys Val Pro Cys Val Lys Glu Gly Asn His Ser Arg Cys Trp
65 70 75 80

Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu
85 90 95

Glu Ser Leu Arg Ser His Val Asp Val Met Val Gly Ala Ala Thr Val
100 105 110

Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu Val
115 120 125

Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Glu
130 135 140

Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GACGGGATCA ATTATGCAAC AGGGAACCTC CCCGGTTGCT CTTTCTCTAT CTTCATCCTG	60
GCACTTCTCT CGTGCCTGAC TGTCCCGGCC TCGGCTCAGC ATTATCGGAA TGTCTCGGGC	120
ATTTACCACG TCACCAACGA CTGCCCGAAC TCCAGCATAG TGTATGAGTC CGACCATCAC	180
ATCTTACACC TACCAGGGTG TGTACCCTGT GTGAAGACTG GGAACACTTC GCGCTGCTGG	240
GTGGCCTTAA CACCTACCGT GGCGCGGCC ATACTTCGG CTCCACTTAT GTCCGTACGG	300
CGGCATGTGG ATCTGATGGT GGGTGCAGCT ACCCTATCGT CTGCCCTCTA CGTTGGAGAC	360
CTCTGCGGGG GTGCCTTCCT AGTGGGGCAG ATGTTCACCT TCCAGCCGCG TCGCCACTGG	420
ACTGTCCAAG ACTGCAACTG TTCCATC	447

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser
1															15
Ile	Phe	Ile	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala
20															30
Gln	His	Tyr	Arg	Asn	Val	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	Cys

35	40	45
Pro Asn Ser Ser Ile Val Tyr Glu Ser Asp His His Ile Leu His Leu		
50	55	60
Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Thr Ser Arg Cys Trp		
65	70	75
Val Ala Leu Thr Pro Thr Val Ala Ala Pro Ile Leu Ser Ala Pro Leu		
85	90	95
Met Ser Val Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr Leu		
100	105	110
Ser Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu Val		
115	120	125
Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Val Gln Asp		
130	135	140
Cys Asn Cys Ser Ile		
145		

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATGAGCACAC TTCCAAAACC CCAAAGAAAA ACCAAAAGAA ATACTAACCG TCGCCCTATG	60
GACGTCAAGT TCCCAGGGCGG CGGCCAGATC GTTGGTGGAG TTTACTTGTGTT GCCGGCGCAGG	120
GGCCCTCGTT TGGGTGTGCG CGCGACGAGA AAGACCTCCG AACGGTCCCA GCCTAGAGGC	180
AGGCGCCAGC CCATACCAAA GGTACGCCAG CCGACAGGCC GTAGCTGGGG TCAACCCGGC	240
TACCCATTGGC CCCTTTATGG CAACGAGGGC TGCGGATGGG CGGGATGGCT CCTGTCCCCC	300
CGCGGGTCTC GTCCTAATTG GGGCCCCAAC GACCCCCGGC GAAGGTCCCG CAACTTGGGT	360
AAGGTCATCG ATACCCTTAC ATNCGGNCTA GCCGACCTCA TGGGGTACAT CCCTGTCTA	420

GGAGGGCCGC TTGGCGGCGT TGCGGCTGCC CTGGCGCATG GCGTTAGGGC AATCGAGGAC 480
GGGGTCAATT ACGCAACAGG GAATCTTCCT GGTTGCTCCT TTTCTATCTT CCTCTTAGCA 540
CTGTTATCGT GCCTCACTAC ACCAGCCTCA GCAATTCAAG TCAAGAACGC CTCTGGGATC 600
TACCATCTTA CCAATGACTG CTCGAACAAC AGCATCGTT TTGAGGCAGGA GACCATGATA 660
CTGCATCTTC CAGGTTGTGT CCCATGTATC AAGGCAGGGA ATGAGTCACG ATGTTGGCTC 720
CCTGTCTCCC CCACCTTAGC CGTCCCCAAC TCATCAGTGC CAATCCACGG GTTTCGCCGA 780
CACGTAGACC TCCTCGTTGG GGCAGCGGCA TTTTGTTCGG CCATGTACAT CGGAGACCTC 840
TGTGGTAGCA TAATCTTGGT AGGGCAGCTT TTTACTTTCA GGCCTAAGTA CCATCAGGTT 900
ACCCAGGATT GTAACTGCTC TATNAACNCT GGCCACGTCA CGGGACACAG GATGGCA 957

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Val Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Xaa

115	120	125
Xaa Leu Ala Asp Leu Met Gly Tyr Ile Pro Val Leu Gly Gly Pro Leu		
130	135	140
Gly Gly Val Ala Ala Ala Leu Ala His Gly Val Arg Ala Ile Glu Asp		
145	150	155
Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile		
165	170	175
Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Ile		
180	185	190
Gln Val Lys Asn Ala Ser Gly Ile Tyr His Leu Thr Asn Asp Cys Ser		
195	200	205
Asn Asn Ser Ile Val Phe Glu Ala Glu Thr Met Ile Leu His Leu Pro		
210	215	220
Gly Cys Val Pro Cys Ile Lys Ala Gly Asn Glu Ser Arg Cys Trp Leu		
225	230	235
Pro Val Ser Pro Thr Leu Ala Val Pro Asn Ser Ser Val Pro Ile His		
245	250	255
Gly Phe Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys		
260	265	270
Ser Ala Met Tyr Ile Gly Asp Leu Cys Gly Ser Ile Ile Leu Val Gly		
275	280	285
Gln Leu Phe Thr Phe Arg Pro Lys Tyr His Gln Val Thr Gln Asp Cys		
290	295	300
Asn Cys Ser Xaa Asn Xaa Gly His Val Thr Gly His Arg Met Ala		
305	310	315

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATGAGCACAC TTCCAAAACC CCAAAGAAAA ACCAAAAGAA ACACCATCCG CCGCCCACAG	60
GACGTCAAGT TCCC GG GTGG CGGCCAGATC GTTGGTGGAG TCTACTTGCT GCCGCGCAGG	120
GGCCCGCGCT TGGGTGTGCG CGCGACGAGA AAGACTTCTG AACGGTCCCA GCCCAGAGGT	180
AGGCGCCAAC CAATACCAA AGTGCACAC CAAACGGGC GTACCTGGC CCAGCCCAGG	240
TACCCCTGGC CTCTTATGG AAATGAGGGC TGTGGTGGG CAGGCTGGCT CCTGTCCCCC	300
CGCGGCTCTC GCCCAAATTG GGGCCAAAC GACCCCCGGC GGAGGTCCCG CAACTGGGT	360
AAAGTCATCG ACACCCTTAC TTGCGGCTTC GCCGACCTCA TGGGTATAT CCCTGTCGTA	420
GGCGCTCCGW TGGGAGGC GT CGCGNGGCC TTGGCGCATG GGGTCANGGN CATCGAGGAC	480
GGNGTAAATT ACGAACAGN GAATCTTCCC GGNNGCTCTN TCTCTATCTT NCTCTGGCA	540
CTTCTCTCGT GCCTTACAAC ACCAGCCTCC GCGGCGCATT ATACCAACAA GTCTGGCTG	600
TACCATCTCA CCAACGACTG CCCCACAGC AGCATCGTT ATGAGGCGGA GACACTGATT	660
TTGCACTTGC CTGGGTGTGT ACCTTGTGTG AAGRTGRACA ATCAATCCCG GTGCTGGGTG	720
CAGGCCTCCC CGACCCTGGC AGTGCCAAC GCGTCTACGC CAGTCACCGG GTTCCGCAA	780
CATGTGGACA TCATGGTGGG CGCTGCCGCG TTCTGTTCAAG CTATGTATGT GGGGGACCTG	840
TGCGGGGGCC TTTTCCTCGT TGGACAGCTC TTCACGCTCA GGCCTCGGAT GCATCAGGTT	900
GTCCAGGAGT GTAACTGTTC CATCTACACA GGGCATATCA CTGGACACCG AATGGCA	957

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Ile			
1	5	10	15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala			

35	40	45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro		
50	55	60
Ile Pro Lys Val Arg His Gln Thr Gly Arg Thr Trp Ala Gln Pro Gly		
65	70	75
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp		
85	90	95
Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro		
100	105	110
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys		
115	120	125
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Xaa		
130	135	140
Gly Gly Val Ala Xaa Ala Leu Ala His Gly Val Xaa Xaa Ile Glu Asp		
145	150	155
Xaa Val Asn Tyr Ala Thr Xaa Asn Leu Pro Xaa Xaa Ser Xaa Ser Ile		
165	170	175
Xaa Leu Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Ala		
180	185	190
His Tyr Thr Asn Lys Ser Gly Leu Tyr His Leu Thr Asn Asp Cys Pro		
195	200	205
Asn Ser Ser Ile Val Tyr Glu Ala Glu Thr Leu Ile Leu His Leu Pro		
210	215	220
Gly Cys Val Pro Cys Val Lys Xaa Xaa Asn Gln Ser Arg Cys Trp Val		
225	230	235
Gln Ala Ser Pro Thr Leu Ala Val Pro Asn Ala Ser Thr Pro Val Thr		
245	250	255
Gly Phe Arg Lys His Val Asp Ile Met Val Gly Ala Ala Ala Phe Cys		
260	265	270
Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu Val Gly		
275	280	285
Gln Leu Phe Thr Leu Arg Pro Arg Met His Gln Val Val Gln Glu Cys		
290	295	300
Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met Ala		
305	310	315

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATGAGCACAC	TTCCTAAACC	TCAAAGAAAA	ACCAAACGAA	ACACCAACCG	TCGCCACAG	60
GACGTCAAGT	TCCC GG GTGG	CGGTCAGATC	GTTGGTGGAG	TTTACTTGTT	GCCGCGCAGG	120
GGCCCTCGTT	TGGGTGTGCG	CGCGACGAGG	AAAAC TTCTG	AACGGTCCCA	GCCCAGGGT	180
AGACGCCAAC	CTATACCGAA	GGTGC GTCAC	CAAACGGGCC	GTACCTGGC	TCAACCCGGG	240
TACCCCTGGC	CTCTTTATGG	GAATGAGGGT	TGTGGCTGGG	CAGGGTGGCT	CCTGTCCCCC	300
CNCGGCTCTC	GCCCTAATTG	GGGCCCTAAT	GACCCCGGN	GGAGGTCCCG	CAACCTGGGT	360
AAGGTCATCG	ATACCCTTAC	TTGNGGSTTC	GCCGACCTCA	TAGAGTACAT	TCC	413

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1															15
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
															30
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala
															45
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro

50	55	60
Ile Pro Lys Val Arg His Gln Thr Gly Arg Thr Trp Ala Gln Pro Gly		
65	70	75
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp		
85	90	95
Leu Leu Ser Pro Xaa Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro		
100	105	110
Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Xaa		
115	120	125
Xaa Phe Ala Asp Leu Ile Glu Tyr Ile		
130	135	

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATGAGCACAC TTCCAAAACC CCAAAGAAAA ACCAAAAGAA ACACAAACCG TCGCCAATG	60
GATGTCAAGT TCCCAGGCGG CGGTCAGATC GTTGGTGGAG TCTACTTGTGTT ACCGCGCAGG	120
GGCCCACGTT TGGGTGTGCG CGCGACGAGG AAGACTTCGG AACGGTCCCA GGCCAGAGGT	180
AGGCGCCAAC CAATACCCAA GGTGCGCCAG AACCAAGGCC GAACCTGGGC TCAGCCTGGG	240
TACCCCTGGC CCCTTTATGG GAACGAGGGC TGCGGCTGGG CGGGGTGGCT CTTGTCCCCC	300
CGTGGCTCTC GCCCGGACTG GGGNCCCAAT GACCCCCGGN GGAGGTCCCG CAACCTGGGT	360
AAGGTCATCG ACACCCCTCAC TTGCGGCTTC GCCGACCTCA TGGAGTACAT CCCTGTCGTT	420
GGCGCCCCCCC TTGGAGGCCT TGCGGCGGAA CTGGNACATG GTGTCAGGGC CATCGAGGAC	480
GGGATAAACT ATGCAACAGG GAATCTTCCT GGTTGCTCTT TCTCTATCTT CCWCTTGGCA	540
CTTCTCTCGT GCCTCACCA GCCTGCCTCC GCACTAAACT ATGCTAACAA GTCTGGGCTG	600

TATCATCTAA CCAATGACTG CCCCAATAGC AGCATTGTGT ATGAGGGCAA TGGCATGATC 660
CTGCATCTCC CGGGTTGCGT CCCCTGCGTG AAGACCGGCA ACCTGACCAA GTGTTGGCTG 720
TCGGCCTCCC CGACATTGGC GGTGCAGAAT GCGTCGGTGT CCATCAGGGG TGTCCGCGAG 780
CACGTGGACC TCTTGGTGGG TGCTGCTGCG TTCTGCTCTG CCATGTACGT GGGCGACTTA 840
TGCGGTGGGC TCTTCTCGT TGGGCAGTTG TTCACGTTCA GACCCAGGAT GTATGAGATC 900
GCCCAGGACT GCAACTGTTG CATCTATGCA GGCCACATCA CTGGGCACCG GATGGCG 957

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Ala Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Val Arg Gln Asn Gln Gly Arg Thr Trp Ala Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asp Trp Xaa Pro Asn Asp Pro
100 105 110

Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Met Glu Tyr Ile Pro Val Val Gly Ala Pro Leu
130 135 140

Gly Gly Val Ala Ala Glu Leu Xaa His Gly Val Arg Ala Ile Glu Asp

145	150	155	160
Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile			
165	170	175	
Phe Xaa Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Leu			
180	185	190	
Asn Tyr Ala Asn Lys Ser Gly Leu Tyr His Leu Thr Asn Asp Cys Pro			
195	200	205	
Asn Ser Ser Ile Val Tyr Glu Ala Asn Gly Met Ile Leu His Leu Pro			
210	215	220	
Gly Cys Val Pro Cys Val Lys Thr Gly Asn Leu Thr Lys Cys Trp Leu			
225	230	235	240
Ser Ala Ser Pro Thr Leu Ala Val Gln Asn Ala Ser Val Ser Ile Arg			
245	250	255	
Gly Val Arg Glu His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys			
260	265	270	
Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu Val Gly			
275	280	285	
Gln Leu Phe Thr Phe Arg Pro Arg Met Tyr Glu Ile Ala Gln Asp Cys			
290	295	300	
Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met Ala			
305	310	315	

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATGAGCACAC TTCCTAAACC ACAAAGAAAA ACCAAAAGAA ACACCAACCC CGGCCACAGG	60
ACGTTAAGTT CCCAGGCGGC GGTCAGATCG TTGGTGGAGT TTACGTGCTA CCACGCAGGG	120

CCCCCCAGTT GGGTGTGCGT GCAGTGCGCA AGACTTCCGA GCGGTCGCAA CCTCGCAGTA 180
GGCGCCAACC CATCCCCAGG GCGCGCCGAA CCGAGGGCAG GTCCTGGGCT CAGCCCGGGT 240
ACCCTTGGCC CCTATATGGG AATGAGGGCT GCGGGTGGGC AGGGTGGCTC CTGTCCCCGC 300
CGGGCTCTC 309

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Xaa Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Gln Leu Gly Val Arg Ala
35 40 45

Val Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Ser Arg Arg Gln Pro
50 55 60

Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Arg
115

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GACGGAATTAA	ATTCGCAAC	AGGGAATTAA	CCTGGTTGCT	CTTTCTCTAT	CTTCCTTCTG	60
GCTTTGTTCT	CATGCTTGCT	TACACCCACA	GCCGGGCTGG	AGTACCGTAA	TGCCTCCGGA	120
CTCTACATGG	TAACTAACGA	CTGCAGTAAC	GGTAGTATCG	TGTATGAGGC	CGGGGATATT	180
ATCCTCCACT	TACCTGGCTG	TGTCCCCTGC	GTACGCTCTG	GCAATACATC	AAGATGCTGG	240
ATCCCTGTGA	GCCCYACCGT	CGCCGTGAAG	TCGCCCTGCG	CCGCCACCGC	CTCTCTCCGC	300
ACGCACGTGG	ATATGATGGT	GGGRGCGGCC	ACCCATATGCT	CAGCTCTCTA	CGTAGGAGAC	360
CTTTGTGGAG	CGCTATTCT	TGTYGGGCAG	GGGTTCTCAT	GGAGACATCG	CCAGCATTGG	420
ACTGTCCAGG	ACTGCAACTG	TTCCATC				447

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Asp	Gly	Ile	Asn	Phe	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser
1				5					10					15	

Ile	Phe	Leu	Leu	Ala	Leu	Phe	Ser	Cys	Leu	Leu	Thr	Pro	Thr	Ala	Gly
					20				25				30		

Leu	Glu	Tyr	Arg	Asn	Ala	Ser	Gly	Leu	Tyr	Met	Val	Thr	Asn	Asp	Cys
						35			40				45		

Ser	Asn	Gly	Ser	Ile	Val	Tyr	Glu	Ala	Gly	Asp	Ile	Ile	Leu	His	Leu
				50				55				60			

Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Ser	Gly	Asn	Thr	Ser	Arg	Cys	Trp
				65				70			75			80	

Ile Pro Val Ser Xaa Thr Val Ala Val Lys Ser Pro Cys Ala Ala Thr

85	90	95
Ala Ser Leu Arg Thr His Val Asp Met Met Val Xaa Ala Ala Thr Leu		
100	105	110
Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ala Leu Phe Leu Xaa		
115	120	125
Gly Gln Gly Phe Ser Trp Arg His Arg Gln His Trp Thr Val Gln Asp		
130	135	140
Cys Asn Cys Ser Ile		
145		

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CTCGACAGTT ACTGAGAATG ACATCCGTGT CGAGGAATCA ATATAACCAAT GTTGTGACTT	60
GGCCCCCGAG GCTCGCAAGG CCATAAAGTC GCTCACCGAG CGGCTGTACA TCGGGGGCCC	120
YCTAACCAAT TCAAAAGGAC AGAACTGCGG CTACCGTCGG TGCCGCGCCA GCGGCGTGCT	180
GACTACCAGC TGCAGCAACA CCCTGACATG CTACTTGAAA GCCAGAGCGG CCTGTCGAGC	240
TGCAAAGCTC CGGGACTGCA CCATGCTCGT GTGCGGGGAT GACCTTGTGTTTATCTGTGA	300
GAGTGCAGGAAG GTCGAGGAAG ACGCGCGAA CCTACGAGCT	340

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Ile Gly Gly Xaa Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Cys Glu Ser Ala Gly Val Glu Glu Asp Ala Ala Asn Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CTCGACAGTT ACTGAGAACG ACATCCGTAC CGAGGRATCA ATCTATCAAT GTTGTGACTT 60
GGCCCCYGAG GCCCGCAAGG CCATAAAGTC GCTCACCGAG CGGCTGTACG TCGGGGGCCC 120
CCTAACCAAT TCAAAGGGGC AGAACTGCGG CTATCGTCGG TGTGCGCTA GCGGCGTGCT 180
GACCACCAGC TGCGGCAACA CCCTCACATG CTACTTGAAA GCCAGGGCGG CCTGTCGAGC 240
TGCAGGACTC CAGGACTGCA CGATGCTCGT GTGCGGAGAC GACCTTGTG 300

GAGCGCGGGA GTCGAGGAGG ACGCGGCAGA CCTACGAGTC

340

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Ser Thr Val Thr Glu Asn Asp Ile Arg Thr Glu Xaa Ser Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu Ala Xaa Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Cys Glu Ser Ala Gly Val Glu Glu Asp Ala Ala Asn Leu Arg
100 105 110

Val

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CTCGACAGTT ACTGAGAACG ACATTCGTGT CGAGGAATCA ATCTACCAAGT GCTGTGACTT 60
GGCCCCCGAG GCCCGCAAGG CCATAAAGTC GCTCACCGAG CGGCTGTATA TCGGGGGTCC 120
CCTAACCAAC TCAAAAGGGC AGAACTGCGG CTACCGTCGG TGCCGCGCCA GCGGCGTGCT 180
GACTACCAGC TGCAGGTAATA CCCTCACATG TTACTTGAAA GCCAGGGCGG CCTGTCGAGC 240
TGCGAAGCTC CAGGACTGCA CAATGCTCGT GTGCGGAGAC GACCTTGTGCG TTATCTGTGA 300
GAGTGCRGGA GTCGAGGAGG ATGCGGCAGAA CCTACGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln
1 5 10 15
Cys Cys Asp Leu Ala Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala
65 70 75 80
Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Cys Glu Ser Xaa Gly Val Glu Glu Asp Ala Ala Asn Leu Arg
100 105 110
Val

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CGTACAGCCT CCAGGACCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG	60
TACACCGGAA TTGCCAGGAC GACCGGGTCC TTTCTTGGAT CAACCCGCTC AATGCCTGGA	120
GATTTGGGCG TGCCCCCGCA AGACTGCTAG CCGAGTAGTG TTGGGTCGCG AAAGGCCTTG	180
TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCGGGAGG TCTCGTAGAC CGTGCACCAC	240
GAGCACGAAT CCTAACCTC AAAGAAAAAC CAAAAGAAAC ACCAACCGCC GCCCACAGGA	300
CGTCAAGTTC CGGGCGGTG GCCAGATCGT TGGTGGAGTC TACGTGCTAC CGCGCAGGGG	360
CCCTAGATTG GGTGTGCGCG CAGCGCGAA GACTCGGAG CGGTCGCAAC CTCGTGGAG	420
GCGCCAACCT ATTCCCAAGG AGCGCCGACC CGAGGGCAGG TCCTGGCGC AGCCCGGGTA	480
CCCCCTGGCCC CTCTATGGTA ACGAGGGCTG CGGGTGGCA GGTNGGCTCC TGTCCCCTCG	540
CGGCTCCCGT CCTAGTTGGG GTCCTACTGA CCCCCGGCGT AGGTCACGCA ATTTGGGTAA	600
GGTCATCGAT ACCCTCACGT GTTGNTTCGC CGACCTCATG GGGTACATAC CG	652

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 138 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	

Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
20							25						30		
Gly	Val	Tyr	Val	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala
	35				40						45				
Ala	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
	50				55					60					
Ile	Pro	Lys	Glu	Arg	Arg	Pro	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly
65			70				75					80			
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Xaa
	85					90						95			
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
	100						105					110			
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys
	115					120					125				
Xaa	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro						
	130					135									

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CTCAACGGTC	ACTGAAGCTG	ATATCCGAAC	AGAGGGAGTCC	ATATACCAAT	GCTGTGACCT	60
GCACCCCGAA	GCACGTGTAG	CCATCAAGTC	TTTGACTGAA	AGGCTGTACG	TCGGGGGGCC	120
CTTGACCAAT	TCAAAAGGGG	AGAACTGCGG	CTATCGCAGA	TGCCGTGCCA	GCGGCGTCTT	180
GACAACCAGC	TGCGGCAACA	CCCTCACCTG	CTATATCAAG	GCCCTAGCAG	CCTGTAGAGC	240
TGCCAAGCTC	CAGGACTGCA	CCATGCTCGT	CTGTGGCGAC	GACCTGGTCG	TGATCTGCGA	300
GAGTGTAGGG	ACCCAGGAGG	ATGCGGCGAG	CCTGCGAGCC			340

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ser Thr Val Thr Glu Ala Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu His Pro Glu Ala Arg Val Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Glu Asn
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Cys Glu Ser Val Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

NTCAACAGTC ACTGAGAGTG ATATCCGTAC AGAGGGAGTCC ATCTACCAAT GCTGTGATCT 60
AGACCCCGAG GCTCGCAAGG CCATAAGGTC CCTCACAGAG AGGCTTTATA TCGGGGGTCC 120
CCTGACAAAC TCAAAAGGGC AGAACTGCGG CTACCGCCGA TGCCGTGCAA GCGGCGTCCT 180
GACGACTAGC TGCAGCAACA CCCTCACCTG TTACATAAAG GCCAGGGCAG CCTGTCGAGC 240
TGCAGAGCTC CAGGATTGCT CAATGCTCGT CTGTGGCGAC GACCTTGTG 300
GATCGAGGGG NTCCANGAGG ATCCGTCGAN NNNNNNNNNNN 340

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Ser Thr Val Thr Glu Ser Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu Asp Pro Glu Ala Arg Lys Ala Ile Arg Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Ile Lys Ala Arg Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Gln Asp Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Cys Glu Ile Glu Gly Xaa Xaa Glu Asp Pro Ser Xaa Xaa Xaa
100 105 110

Xaa

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

CGTAGACCGT	GCACCATGAG	CACGAATCCT	AAACCTCAA	AAAAACCAA	ACGTAACATC	60
AACCGCCGCC	CACAGGACGT	CAAGTTCCCG	GGCGGTGGCC	AGATCGTCGG	TGGAGTTTAC	120
CTGTTGCCGC	GCAGGGGCC	TAGATTGGGT	GTGCGCGCGA	CTAGGAAGAC	TTCCGAGCGG	180
TCGCAACCTC	GTGGGAGGCG	ACAGCCTATC	CCCAAGGCTC	GCCGATCCGA	GGGCAGGTCC	240
TGGGCTCAGC	CCGGGTACCC	TTGGCCCCCTC	TATGGCAATG	AGGGCATGGG	TTGGGCAGGG	300
TGGCTCCTGT	CCCCCATGG	CTCCCGGCCT	AGTTGGGGCC	CTTCAGACCC	CCGGCGTAGG	360
TCGCGTAATT	TGGGTAAGGT	CATCGATACC	CTCACATGCG	GCTTCGCCGA	CCTCATGGGG	420
TACATTCCGC	TCGTGGCGC	CCCCCTAGGG	GGCGTTGCCA	GGGCCCTGGC	GCAAGGCTTC	480
CGGGATCTAC	CACGTCACCA	ACGATTGTT	CAATGGGAGC	ATTGTGTATG	AGGCGGAAGG	540
CATGATCATG	CATCTCCCCG	GGTGCCTGCC	CTGCGTTCGG	GAAGGTAATA	TCTCTCGTTG	600
CTGGGTACCG	TTTCCCCCA	CGCTCGCAGC	CAGGAATGCT	AGCGTCCCCA	CTCAGGCAAT	660
TCGGCGACAC	GTCGACTTGC	TTGTTGGGGC	GGCCACACTC	TGTTCTGCTA	TGTATGTGGG	720
GGACCTCTGT	GGGTCCGTCT	TCCTCGTCGG	CCAACTGTT	ACCTTCACAW	CCCGCCAGNA	780
CTACACAGTG	CAAGACTGCA	ATTGTTCCAT	CTACCCGGC	CATATAACGG	G	831

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Ile Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro His Gly Ser Arg Pro Ser Trp Gly Pro Ser Asp Pro
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
130 135 140

Gly Gly Val Ala Arg Ala Leu Ala Gln Gly Phe Arg Asp Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

NNNNNNNGTC ACTGAGAGTG ATATCCGTGT CGAGGARTCA ATTTACCAAT GCTGTGACCT 60
GGCCCCCGAG GCTCGCGTAG CCATAAAGTC GCTCACTGAG CGGCTATATG TCGGGGGCCC 120

TCTCACCAAC TCAAAAGGAC AGAACTGCGG CTATGCCGG TGCCGTGCGA GCGGTGTGCT	180
GACTACTAGC TGCAGTAACA CCCTCACATG CTACCTGAAA GCCGCCGCGG CCTGTCGAGC	240
TGCAAAGCTC CGGGAAATGCA CAATGCTCGT GTGTGGCGAC GACCTCGTCG TTATCTGTGA	300
GAGTGCAGGGG GTCCAGGAGG ATGCTGCAAG CCTNNNNNNNN	340

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Xaa Xaa Val Thr Glu Ser Asp Ile Arg Val Glu Xaa Ser Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Val Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ala Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Arg Glu Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Cys Glu Ser Ala Gly Val Gln Glu Asp Ala Ala Ser Xaa Xaa
100 105 110

Xaa

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CTCGACAGTC ACAGAGAGAG ATATAAGNAC TGAGGAGTCC ATATACCAGG CTTGTTCC	60
ACCCGAGCAG GCCAGAACTG CCATACACTC ATTGACTGAG AGACTCTACG TAGGAGGGCC	120
CATGATGAAC AGCAAAGGGC AATCCTGCGG ATACAGGCAT TGCCGCGCCA GCGGAGTGCT	180
CACCACCAGT ATGGGAATA CCATCACGTG CTACATCAAG GCCCTAGCGG CTTGTAAAGC	240
AGCAGGAATA GTGGCCCCCA CCATGCTGGT GTGCGGCGAT GACCTAGTTG TCATCTCAGA	300
GAGTCAGGGA GTCGAGGAGG ACGACCGGAA CCTGANNNN	340

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Ser Thr Val Thr Glu Arg Asp Ile Xaa Thr Glu Glu Ser Ile Tyr Gln			
1	5	10	15
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr			
20	25	30	
Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser			
35	40	45	
Cys Gly Tyr Arg His Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met			
50	55	60	
Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala			
65	70	75	80
Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val			
85	90	95	
Val Ile Ser Glu Ser Gln Gly Val Glu Glu Asp Asp Arg Asn Leu Xaa			
100	105	110	

Xaa

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTCAACCGTC ACAGAGAGGG ATATAAGAAC TGAGGAGTCC ATATAACCTGG CCTGCTCCTT	60
ACCCGAGCAG GCCCGGACTG CCATACATTC ATTAACGTAG AGACTTTACG TGGGAGGGCC	120
CATGATGAAC AGCAAAGGGC AGTCCTGCGG ATACAGGCCT TGCCGCGCTA GCGGAGTGCT	180
CACCACCACT ATGGGGAAACA CCATCACGTG TTATGTGAAA GCCCTCGCAG CTTGTAAAGC	240
TGCGGGCATT GTTGCCCCCA CGATGCTGGT GTGCGGCGAT GACCTGGTTG TCATCTCAGA	300
GAGTCAGGGG GCTGAGGGAGG ACGAGCGAAA CCTGAGAGTC	340

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
1 5 10 15

Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser

35

40

45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
50 55 60

Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys Lys Ala
65 70 75 80

Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ser Glu Ser Gln Gly Ala Glu Glu Asp Glu Arg Asn Leu Arg
100 105 110

Val

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CTCAACAGTC GCGGAGAGAG ACATCAGGAC CGAGGAGTCC ATTTACCTTG CCTGCTCCTT 60
ACCCGAGCAA GCCCGAACTG CCATACATTC ATTGACTGAG AGACTTTACG TAGGAGGGCC 120
CATGATGAAC AGCAAGGGAC AGTCCTGCGG TTACAGACGT TGCCGCGCCA GCGGAGTGCT 180
CACCACCAGC ATGGGGAATA CCATCACATG CTATGTGAAG GCATTAGCTG CCTGCAAAGC 240
TGCAGGCATC GTTGCTCCCA CGATGCTGGT TTGTGGCGAC GATCTGGTCA TCATCTCAGA 300
GAGTCAGGGA ACCGAGGAGG ATGAGCGGAA CCTGAGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Ser Thr Val Ala Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
1 5 10 15

Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
50 55 60

Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys Lys Ala
65 70 75 80

Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Ile Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg
100 105 110

Val

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CGNACANCCT CCAGGCCCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG 60

TACACCGGAA TTGCCGGAA GACTGGGTCC TTTCTTGGAT AAACCCACTC TATGCCCGGC 120

CATTGGGCG TGCCCCCGCA AGACTGCTAR CCGAGTAGCG TTGGGTTGCG AAAGGCCTTG 180

TGGTACTGCC	TGATAGGGTG	CTTGCAGTG	CCCCGGGAGG	TCTCGTAGAC	CGTGCATCAT	240
GAGCACAAAT	CCTAACCTC	AAAGAAAAAC	CAAAAGAAC	ACTAACGCC	GCCCACAGGA	300
CGTTAAGTTC	CGGGCGGTG	GCCAGATCGT	TGGCGGAGTA	TACTTGTG	CNTGCAGGGG	360
NCCCAGGTNG	NGTNTATGCG	CAACGANGAA	GACTIONCGAA	CAGTCCCAGC	CACGTGGGAG	420
GCGCCAGCCC	ATCCCGAAAG	ATCGGNGCAC	CACTGGCAAG	TCCTGGGAC	GTCCAGGATA	480
TCCCTGGCCC	CTGTATGGGA	ACGAGGGCCT	CGGGTGGGCA	GGGTGGCTCC	TGTCCCCCG	540
GGGCTCCCGC	CCGTCATGGG	GCCCCACGGA	CCCCCGGCAT	AGGTCGCGCA	ACTTGGTAA	600
GGTCATCGAT	ACCCTCACGT	NCGGCTTTNC	CGACCTCATG	GGGTACATTC	CCGTCGTTGG	660
CGCCCCAGTA	GGNGGCGTCG	CCAGAGCTCT	CGCGCATGGC	GTGAGAGTCC	TGGAGGACGG	720
GATAAACTAT	GAAACAGGGA	ACCTCCCCGG	TTGCTCTTTC	TCTATCTCCC	TCCTTGCTCT	780
TCTGTCCTGA	ATTACCGNGC	CAGTTCTGC	TGTGGAAATC	AAAAACACCA	GMAACACATA	840
CATGGTGACT	AACGACTGTT	CAAACAGYAG	CATCACCTGG	CAGCTTNNGN	NCGCGGTGCT	900
TCACGTTCCCT	GGATGCGTCC	CCTGTGAACG	AGAGGGCAAC	AGTTCCCGGT	GCTGGATTCC	960
AGTCACGCC	RACGTAKNCG	TGAGCCGACC	TGGTGCCCTA	ACCGAGGGTT	TGCGATCGCA	1020
CATCGACACC	ATCGTAGCGT	CCGCAACATT	TTGTTCTGCC	CTCTACATAG	GGGATGTATG	1080
TGGCGCGATA	ATGATAGCTG	CCCAAGTGGT	CATCGTCTCG	CCGGAGCATC	ATCACTTTGT	1140
CCAGGACTGT	AACTGTTCCA	TCTACCCGGG	CCACATAACG	GGGCCTCGTA	TGTNG	1195

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1															15

Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
															30
20															

Gly	Val	Tyr	Leu	Leu	Xaa	Cys	Arg	Xaa	Pro	Arg	Xaa	Xaa	Cys	Ala	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

35

40

45

Thr Xaa Lys Thr Xaa Glu Gln Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

Ile Pro Lys Asp Arg Xaa Thr Thr Gly Lys Ser Trp Gly Arg Pro Gly
 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110

Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Xaa
 115 120 125

Gly Phe Xaa Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
 130 135 140

Xaa Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160

Gly Ile Asn Tyr Glu Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175

Ser Leu Leu Ala Leu Leu Ser Ile Thr Xaa Pro Val Ser Ala Val Glu
 180 185 190

Ile Lys Asn Thr Xaa Asn Thr Tyr Met Val Thr Asn Asp Cys Ser Asn
 195 200 205

Xaa Ser Ile Thr Trp Gln Leu Xaa Xaa Ala Val Leu His Val Pro Gly
 210 215 220

Cys Val Pro Cys Glu Arg Glu Gly Asn Ser Ser Arg Cys Trp Ile Pro
 225 230 235 240

Val Thr Pro Xaa Val Xaa Val Ser Arg Pro Gly Ala Leu Thr Glu Gly
 245 250 255

Leu Arg Ser His Ile Asp Thr Ile Val Ala Ser Ala Thr Phe Cys Ser
 260 265 270

Ala Leu Tyr Ile Gly Asp Val Cys Gly Ala Ile Met Ile Ala Ala Gln
 275 280 285

Val Val Ile Val Ser Pro Glu His His His Phe Val Gln Asp Cys Asn
 290 295 300

Cys Ser Ile Tyr Pro Gly His Ile Thr Gly Pro Arg Met Xaa
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

ATCCACAGTC ACTGAAAGAG ACATCAGAGT TGAAGAGTCC GTTTATCTGT CCTGTTCACT	60
TCCCGAGGAG GCCCGAGCTG CCATACACTC ACTAACTGAG AGGCTGTACG TGGGAGGTCC	120
CATGCAGAAC AGCAAGGGC AATCCTGCAG ATACAGGCGC TGCCGCGCCA GCGGGGTGCT	180
CACCACTAGC ATGGGAATA CTCTCACATG CTACTTGAAG GCCCAGGCGG CCTGCAGGGC	240
CGCGGGCATT GTTGCACCCA CAATGCTGGT GTGTGGCGAC GACCTGGTCG TCATCTCAGA	300
GAGTCAGGGG ACTGAGAGGG ACGAGAACAA CCTGAGACCT	340

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Val	Glu	Glu	Ser	Val	Tyr	Leu
1				5					10			15			

Ser	Cys	Ser	Leu	Pro	Glu	Glu	Ala	Arg	Ala	Ala	Ile	His	Ser	Leu	Thr
			20					25				30			

Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Gln	Asn	Ser	Lys	Gly	Gln	Ser
				35			40		45						

Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Thr	Thr	Ser	Met
				50			55			60					

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65 70 75 80

Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ser Glu Ser Gln Gly Thr Glu Arg Asp Glu Asn Asn Leu Arg
100 105 110

Pro

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

CTCAACAGTC ACGGAGAGGG ACATCAGGAA TGAGGGAGTCC ATATTCTGG CCTGCTCGTT 60

GCCCGAGGAG GCCCGGACTG TCATACATTC GCTCACTGAG AGACTCTACA TAGGCGGGCC 120

GATGATGAAC AGCAAAGGCC AGTCCTGTGG ATACAGGCGT TGTCGCGCCA GCGGGGTGT 180

CACCACTAGC ATGGGCAATA CCATCACGTG CTATGTAAA GCCATGGCAG CTTGCAGAGC 240

TGCCGGGATT GACGCCCCA CAATGTTGGT ATGTGGCGAC GACCTGGTGG TCATCTCAGA 300

GAGTCAGGGG ACCGAGGAGG ACGAGCGAAA TCTGAGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ser Thr Val Thr Glu Arg Asp Ile Arg Asn Glu Glu Ser Ile Phe Leu
 1 5 10 15
 Ala Cys Ser Leu Pro Glu Glu Ala Arg Thr Val Ile His Ser Leu Thr
 20 25 30
 Glu Arg Leu Tyr Ile Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
 35 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
 50 55 60
 Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Met Ala Ala Cys Arg Ala
 65 70 75 80
 Ala Gly Ile Asp Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg
 100 105 110
 Val

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CTCTTGACTC TACTGTCACT GAACAGGATA TCAGGGTAGA AGAAGAAATA TACCAATGTT	60
GTGACCTTGA GCCGGAGGCT AGACGGGCAA TCAAATCGCT CACGGAACGG CTTTACGTTG	120
GAGGTCCCAT GTTCAACAGC AAGGGGCTCA AATGCGGATA TCGCCGTTGC CGTGCTAGCG	180
GTGTATTGCC CACTAGCTAC GGTAATACAA TCACCTGCTA CATCAAGGCC AGAGCGGCTG	240
CTCGAGCTGC GGGCCTTCAA GACCCATCAT TCCTTGTCTG CGGAGATGAT TTGGTGTTAG	300
TGGCTGAGAG TTGCGKCGTT GATGAGGAGG ATAGGGCAGC	340

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Leu Lys
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Tyr
50 55 60

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Arg Ala Ala Ala Arg Ala
65 70 75 80

Ala Gly Leu Gln Asp Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Val Ala Glu Ser Cys Xaa Val Asp Glu Glu Asp Arg Ala Ala Leu
100 105 110

Arg

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CTCCACTGTA ACCGAAAAGG ACATCAGGCC CGAGGAAGAG GTCTATCAGT GTTGTGACCT	60
GGAGCCCGAA GCTCGCAAGG TTATTACCGC CCTCACAGAA AGACTCTACG TGGGCGGCC	120
CATGCACAAC AGCAAGGGAG ACCTTTGTGG GTATCGGAGA TGCCGCGCAA GCGGCGTCTA	180
CACGACCAGC TTCGGAAACA CACTGACGTG CTACCTCAAA GCCTCAGCTG CTATTAGAGC	240
GGCAGGGCTG AGAGACTGCA CCATGCTGGT TTGCGGTGAC GACTTGGTCG TCATCGCTGA	300
GAGCGATGGC GTAGAGGAGG ATAACCGAGC CCTCCNAGCC	340

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Ser Thr Val Thr Glu Lys Asp Ile Arg Pro Glu Glu Glu Val Tyr Gln			
1	5	10	15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr			
20	25	30	
Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu			
35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Ser Phe			
50	55	60	
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala			
65	70	75	80
Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val			
85	90	95	
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Asn Arg Ala Leu Xaa			
100	105	110	
Ala			

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

CTCCACGGTG ACTGAAAAGG ACATCAGGGT CGAGGAAGAG ATCTATCAAT GTTGTGACCT	60
GGARCCCGAA GCCCGCAAAG CAATATCCGC CCTCACAGAG AGRCTCTACT TGGGCGGCC	120
CATGTATAAC AGCAAAGGGG AGCTCTGCGG GTATCGGAGG TGCCGCGCGA GCGGAGTGT	180
CACCAACAAGT TTCGGGAACA CAGTGACCTG CTATCTTAAG GCCACCGCAG CTACCAGGGC	240
TGCAGGCCTA AAAGACTGCA CCATGCTGGT CTGCGGTGAC GACTTGGTCG TCATCGCCGA	300
GAGCGAGGGC GTAGAGGAGG ATTCCCAACC CCTCCGAGCC	340

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln			
1	5	10	15
Cys Cys Asp Leu Xaa Pro Glu Ala Arg Lys Ala Ile Ser Ala Leu Thr			
20	25	30	
Glu Xaa Leu Tyr Leu Gly Gly Pro Met Tyr Asn Ser Lys Gly Glu Leu			
35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe			
50	55	60	
Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala			
65	70	75	80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Glu Gly Val Glu Glu Asp Ser Gln Pro Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTCCACCGTA ACCGAAAGGG ACATCAGGGT CGAGGAGGAG GTCTATCAGT GTTGTGATCT	60
GGAGCCAGAG GCCCGCAAGG CAATATCCGC CCTCACGGAG AGACTCTATG TGGGCGGTCC	120
CATGTTAAC AGCAAGGGAG ACCTATGTGG CTACCGCAGG TGCCGCGCAA GCGGCGTCTA	180
CACCACCAGC TTCGGAAACA CACTGACCTG CTACCTCAAG GCCACGGCCG CTACCAGAGC	240
GGCCGGCCTG AAGGATTGCA CAATGCTGGT TTGCGGGGAC GACCTGGTCG TCATCGCAGA	300
GAGCGATGGC GTGGACGAGG ACCGCCGAGC CCTCCAAGCT	340

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln

1	5	10	15												
Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Ala	Ile	Ser	Ala	Leu	Thr
			20				25				30				
Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	Asp	Leu
			35				40			45					
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Tyr	Thr	Thr	Ser	Phe
			50			55				60					
Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Thr	Ala	Ala	Thr	Arg	Ala
	65			70			75			80					
Ala	Gly	Leu	Lys	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
			85				90			95					
Val	Ile	Ala	Glu	Ser	Asp	Gly	Val	Asp	Glu	Asp	Arg	Arg	Ala	Leu	Gln
			100				105			110					
Ala															

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

CTCAACAGTC	ACAGAGCGCG	ATGTCCAGAC	GGAGCATGAC	ATCTACCAGT	GCTGTAAGTT	60
GGAGCCCCGCA	GCACGGACAG	CCATCACATC	GCTTACTGAC	CGATTGTACT	NCGGTGGTCC	120
CATGTNTAAC	TCTAAAGGTC	AGGCATGTGG	ATACCGTAGG	TGCAGGGCCA	GTGGCGTCTT	180
GACCACCATC	CTGGCCAATA	CTCTGACTTG	CTACTTGAAA	GCTCAGGCAG	CATGCAGAGC	240
TGCCGGGCTG	AAGGACTTTG	ACATGTTGGT	CTGGCGAGAC	GACCTTGTAG	TTATTTCGGA	300
GAGTTTGGGG	GTCTCGGAGG	ACACTAGTGC	ACTGCGAGCT			340

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ser Thr Val Thr Glu Arg Asp Val Gln Thr Glu His Asp Ile Tyr Gln
1 5 10 15

Cys Cys Lys Leu Glu Pro Ala Ala Arg Thr Ala Ile Thr Ser Leu Thr
20 25 30

Asp Arg Leu Tyr Xaa Gly Gly Pro Met Xaa Asn Ser Lys Gly Gln Ala
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ile Leu
50 55 60

Ala Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65 70 75 80

Ala Gly Leu Lys Asp Phe Asp Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ser Glu Ser Leu Gly Val Ser Glu Asp Thr Ser Ala Leu Arg
100 105 110

Ala

- (2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CTCGACAGTC ACCGAGCGCG ACATCCRCAC CGAGCACGAC ATCTACCAAT GCTGCCAACT 60
TGACCCGGTG GCACGCAAGG CTATTACATC TCTGACTGAG CGGCTGTACT GCGGWGGGCC 120
CATGATGAAC TCCCCTGGTC AATCATGTGG ATACCGTAGG TGCCGAGCCA GTGGCGTGCT 180
CACCACGAGC TTGGGCAATA CCCTAACATG CTATTTGAAA GCACAAGCAG CGTGTAGGGC 240
AGCAAAGCTC AAAAACTATG ACATGTTAGT CTGCGGAGAC GATCTAGTCG TTATCGCGGA 300
GAGTGGAGGA GTCTCTGAGG ATGTTGACGC CCTGCGAGCA 340

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Ser Thr Val Thr Glu Arg Asp Ile Xaa Thr Glu His Asp Ile Tyr Gln
1 5 10 15

Cys Cys Gln Leu Asp Pro Val Ala Arg Lys Ala Ile Thr Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Cys Xaa Gly Pro Met Met Asn Ser Arg Gly Gln Ser
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Leu
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Lys Asn Tyr Asp Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Gly Gly Val Ser Glu Asp Val Asp Ala Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CTCCTCCGTC	ACGGAGCGTG	ACATCCGCAC	TGAACACGAC	ATCTATCAGT	GCTGCCAATT	60
AGATCCGGTA	GCACGGAAAG	CCATTACATC	TCTTACTGAG	CGGCTGTACT	GCGGCGGCC	120
CATGTACAAC	TCTCGAGGTC	AGTCATGTGG	GTACCGCAGG	TGCCGGGCTA	GTGGTGTCTT	180
CACCACAAGC	TTGGGCAACA	CCATGACATG	CTACCTGAAG	GCTCAGGCAG	CTTGTAGGGC	240
AGCRAAGCTC	AAAAACTTTG	ACATGTTGGT	CTGCGGAGAC	GACCTAGTCG	TTATTGCTGA	300
GAGCGGAGGA	GTCCCTGAGG	ATGCCGGGGC	CCTGCGAGTC			340

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Ser	Ser	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	His	Asp	Ile	Tyr	Gln
1				5					10					15	
Cys	Cys	Gln	Leu	Asp	Pro	Val	Ala	Arg	Lys	Ala	Ile	Thr	Ser	Leu	Thr
			20					25				30			
Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Tyr	Asn	Ser	Arg	Gly	Gln	Ser
			35				40				45				
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Phe	Thr	Thr	Ser	Leu
			50				55				60				
Gly	Asn	Thr	Met	Thr	Cys	Tyr	Leu	Lys	Ala	Gln	Ala	Ala	Cys	Arg	Ala
			65				70			75			80		
Xaa	Lys	Leu	Lys	Asn	Phe	Asp	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val

85	90	95
Val Ile Ala Glu Ser Gly Gly Val Pro Glu Asp Ala Gly Ala Leu Arg		
100	105	110
Val		

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

ATCCACAGTC ACGGGCGCG ACATACGCAC AGAACNAGAC ATTTACCTGT CCTGCCAGCT	60
CGACCCAGAG GCCCGGAAAG CCATAAAGTC TCTCACTGAG AGGCTCTATG TCGGGGGCCC	120
TATGTACAAC TCAAAGGGCC AACTCTGTGG TCAACGCCGA TGCCGAGCAA GCGGAGTACT	180
CCCCACAAGC ATGGGTAACA CCATCACATG CTTCCTGAAG GCAACCGCCG CTTGCCGAGC	240
AGCCGGCTTT ACAGATTATG ACATGTTGGT CTGCGGAGAC GATTTGGTTG TCGTAACTGA	300
GAGTGCTGGA GTCAACGAGG ATATCGCTAA CCTGCGAGCC	340

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Ser Thr Val Thr Gly Arg Asp Ile Arg Thr Glu Xaa Asp Ile Tyr Leu	
1	5
	10
	15

Ser Cys Gln Leu Asp Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Leu
 35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Met
 50 55 60

Gly Asn Thr Ile Thr Cys Phe Leu Lys Ala Thr Ala Ala Cys Arg Ala
 65 70 75 80

Ala Gly Phe Thr Asp Tyr Asp Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Val Val Thr Glu Ser Ala Gly Val Asn Glu Asp Ile Ala Asn Leu Arg
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CTCCACTGTC ACTGAGCAGG ACATCAGGGT AGAACTTCC ATCTTCAGG CCTGTGACCT	60
CAAGGACGAG GCTAGGAGGG TGATAACTTC ACTCACGGAG CGGCTTACT GTGGTGGTCC	120
TATGTTCAAC AGCAAGGGAC AACACTGCGG TTACCGCCGC TGCCGTGCTA GTGGGGTGCT	180
ACCCACCAGC TTCGGGAACA CAATCACCTG TTACATCAA GCAAAGGCAG CTACCAAAGC	240
TGCCCGAATT AAAATCCAT CATTCTTGT CTGCGGAGAT GACTTGGTCG TGATTGCTGA	300
GAGTGCAGGG ATCGATGAGG ACAAGAGCGC CTTGAGAGCT	340

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Leu Ser Ile Phe Gln
1 5 10 15

Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe
50 55 60

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala
65 70 75 80

Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Lys Ser Ala Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CTCTACCGTC ACAGAGAGGG ACATACGGAC AGAAGAATCC ATCTATCTGT CTTGTCAATT 60

GCCTGAAGAG GCCCGGAAAG CCATTAATC GCTGACAGAG AGACTATACG TGGGCGGCCC 120
GATGGAAAAC AGCAAGGCC AGGCTTGCAG ATATAGGCGT TGCCGCGCAA GCGGGGTATT 180
CACCACAAGC TTGGGAAACA CCATGACTTG TTACATCAA GCTAAAGCGG CTTGTAAAGC 240
CGCTGGCATT GTAGACCCGG TGATGCTCGT GTGCGGTGAC GACCTAGTGG TCATCTCAGA 300
AAGCAAGGGG GTGGAGGAGG ACCAGCGGGA CCTACGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
1 5 10 15
Ser Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
50 55 60
Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Lys Ala Ala Cys Lys Ala
65 70 75 80
Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Arg
100 105 110
Val

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTCCACTGTC ACTGAGAGAG ACATACGGAC AGAAGAATCC ATCTAYYTGG CTTGTCAATT	60
GCCCCGAAGAG GCCCCGAAGG CCATTAAATC ACTGACAGAG AGACTATAACG TGGGCGGCCC	120
GATGGAAAAC AGCAAAGGCC AGGCCTGCGG ATATAGGCCT TGCCGCGCAA GCGGGGTATT	180
CACCACAAGC TTGGGGAACA CCATGACTTG TTACATCAAG GCCAARGCAG CTTGTAAAGC	240
YGCTGGCATT GTTGACCCGG TGATGCTCGT GTGCGGCGAC GACCTAGTGG TCATCTCAGA	300
GAGCAAGGGG GTAGAGGAGG ACCAGCGAGA CCTAC	335

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Xaa Xaa			
1	5	10	15
Ala Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr			
20	25	30	
Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala			
35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu			
50	55	60	
Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Xaa Ala Ala Cys Lys Xaa			
65	70	75	80
Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val			
85	90	95	

Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Xaa
100 105 110

Xaa

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CGTACAGCCT CCAGGACCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG	60
TACACCGGAA TTGCCGGAA GACTGGGTCC TTTCTTGGAT TAACCCACTC TATGCCCGGA	120
GATTTGGGCG TGCCCCCGCA AGACTGCTAG CCGAGTAGCG TTGGGTTGCG AAAGGCCTTG	180
TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCGGGAGG TCTCGTAGAC CGTGCACCAT	240
GAGCACGAAT CCTAACCTC AAAGACAAAC CAAAAGAAAC ACCAACCGCC GCCCACAGGA	300
CGTTAAGTTC CGGGCGGTG GCCAGATCGT TGGCGGGGTG TACTTGTTC CGCGCAGGGG	360
CCCCAGAGTG GGTGTGCGCG CGACGAGAAA GACCTCGGAG CGGTCCCAGC CGCGTGGGAG	420
GCGCCAACCT ATCCCCAAGG TTAGGCGCAC CACCGGCCGT T	461

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Met Ser Thr Asn Pro Lys Pro Gln Arg Gln Thr Lys Arg Asn Thr Asn

1	5	10	15												
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
		20				25							30		
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Val	Gly	Val	Arg	Ala
		35			40		45								
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
		50			55		60								
Ile	Pro	Lys	Val	Arg	Arg	Thr	Thr	Gly	Arg						
		65			70										

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CTCTACTGTC	ACAGAGAGGG	ATATACGAAC	AGAGGAATCC	ATYTATCTGG	CTTGTCAATT	60
GCCCGAAGAG	GCCCGGAAGG	CCATCAAATC	ACTGACAGAG	AGACTATAACG	TGGCGGGCCC	120
GATGGAAAAC	AGCAAGGGCC	AGGCCTGCGG	ATACAGGCGT	TGCCGCGCAA	GCGGGGTATT	180
CACCACAAGC	TTGGGGAACA	CCATGACTTG	TTACATCAA	GCCAAGGCAG	CTTGTAAAGC	240
CGCTGGCATT	GTTGACCCAG	TGATGCTCGT	GTGCGGCGAC	GACCTAGTGG	TCATCTCAGA	300
AAGCAAGGGG	GTGGAGGAGG	ACCAACGAGA	CCTACGANTC			340

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Xaa Tyr Leu
1 5 10 15

Ala Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Lys Ala Ala Cys Lys Ala
65 70 75 80

Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Arg
100 105 110

Xaa

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ala Arg Gln Ser Asp Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

Glu Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

Ala Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Asp Arg Arg Thr Thr Gly Lys Ser Trp Gly Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Asp Arg Arg Ala Thr Gly Arg Ser Trp Gly Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Asp Arg Arg Ala Thr Gly Lys Ser Trp Gly Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Val Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Val Arg His Gln Thr Gly Arg Thr Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Arg Gln Asn Gln Gly Arg Thr Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

Val Arg Arg Thr Thr Gly Arg Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Val Arg Arg Thr Thr Gly Arg Thr Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Tyr Glu Val His Ser Thr Thr Asp Gly Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Val Glu Val Lys Asn Thr Ser Gln Ala Tyr Met Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Ile Gln Val Lys Asn Asn Ser His Phe Tyr Met Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Val Gln Val Lys Asn Thr Ser Thr Met Tyr Met Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Gln Val Lys Asn Thr Ser His Ser Tyr Met Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Val Gln Val Ala Asn Arg Ser Gly Ser Tyr Met Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Val Glu Ile Lys Asn Thr Xaa Asn Thr Tyr Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Val Glu Ile Lys Asn Thr Ser Asn Thr Tyr Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Ile Asn Tyr Arg Asn Val Ser Gly Ile Tyr Tyr Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Ile Asn Tyr Arg Asn Thr Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Ile Asn Tyr His Asn Thr Ser Gly Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

Ile Gln Val Lys Asn Ala Ser Gly Ile Tyr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Ala His Tyr Thr Asn Lys Ser Gly Leu Tyr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Leu Asn Tyr Ala Asn Lys Ser Gly Leu Tyr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Leu Glu Tyr Arg Asn Ala Ser Gly Leu Tyr Met Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Ile Tyr Glu Met Asp Gly Met Ile Met His Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Ile Tyr Glu Met Ser Gly Met Ile Leu His Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

Val Tyr Glu Ala Lys Asp Ile Ile Leu His Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

Val Trp Gln Leu Xaa Asp Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

Val Trp Gln Leu Arg Asp Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Ile Trp Gln Met Gln Gly Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

Val Trp Gln Leu Lys Asp Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

Val Trp Gln Leu Glu Glu Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

Thr Trp Gln Leu Xaa Xaa Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Val Tyr Glu Ala Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

Val Tyr Glu Ala Asp His His Ile Leu Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 150:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

Val Phe Glu Ala Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

Val Tyr Glu Ser Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Val Phe Glu Glu Thr Met Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Val Tyr Glu Ala Glu Thr Leu Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Val Tyr Glu Ala Asn Gly Met Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

Val Tyr Glu Ala Gly Asp Ile Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Val Arg Glu Asp Asn His Leu Arg Cys Trp Met Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Met Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Ile Arg Glu Gly Asn Ile Ser Arg Cys Trp Val Leu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

Glu Asn Ser Ser Gly Arg Phe His Cys Trp Ile Pro Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Glu Arg Ser Gly Asn Arg Thr Phe Cys Trp Thr Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

Glu Leu Gln Gly Asn Lys Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Glu Arg His Gln Asn Gln Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

Glu Trp Lys Asp Asn Thr Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Glu Arg Glu Gly Asn Ser Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Val Arg Glu Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Val Arg Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

Val Arg Val Gly Asn Gln Ser Ser Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Val Lys Glu Gly Asn His Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Val Lys Thr Gly Asn Thr Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Ile Lys Ala Gly Asn Glu Ser Arg Cys Trp Leu Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Val Lys Xaa Xaa Asn Gln Ser Arg Cys Trp Val Gln Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Val Lys Thr Gly Asn Leu Thr Lys Cys Trp Leu Ser Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Val Arg Ser Gly Asn Thr Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Val Lys Asn Ala Ser Val Pro Thr Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Val Lys Asp Ala Asn Val Pro Thr Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

Ala Arg Ile Ala Asn Ala Pro Ile Asp Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Val Ser Lys Pro Gly Ala Leu Thr Lys Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

Val Ser Arg Pro Gly Ala Leu Thr Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Val Asn Gln Pro Gly Ala Leu Thr Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Val Ser Gln Pro Gly Ala Leu Thr Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

Val Ser Arg Pro Gly Ala Leu Thr Glu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Ala Pro Tyr Ile Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Ala Pro Tyr Thr Ala Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Ala Pro Ile Leu Ser Ala Pro Leu Met Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Val Pro Asn Ser Ser Val Pro Ile His Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Val Pro Asn Ala Ser Thr Pro Val Thr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

Val Gln Asn Ala Ser Val Ser Ile Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Val Lys Ser Pro Cys Ala Ala Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Ser Pro Arg Met His His Thr Thr Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Ser Pro Arg Leu Tyr His Thr Thr Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Thr Ser Arg Arg His Trp Thr Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Ala Pro Lys Arg His Tyr Phe Val Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Ser Pro Gln Tyr His Thr Phe Val Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Ser Pro Gln His His Asn Phe Ser Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Ser Pro Gln His His Ile Phe Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Ser Pro Glu His His Phe Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Arg Pro Arg Arg His Trp Thr Ala Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

Gln Pro Arg Arg His Trp Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Arg Pro Arg Arg His Trp Thr Thr Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

Gln Pro Arg Arg His Trp Thr Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 204:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Arg Pro Lys Tyr His Gln Val Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

Arg Pro Arg Met His Gln Val Val Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Arg Pro Arg Met Tyr Glu Ile Ala Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

Arg His Arg Gln His Trp Thr Val Gln Asp
1 5 10